REMARKS AND ARGUMENTS

Election/ Restriction

Applicant acknowledges that Examiner has made the restriction requirement of previous office action final. Applicant however, maintains the arguments of previous office action reply and **respectfully petitions Director for a review of the restriction requirement under 37 CFR 1.144.**

The restriction requirement made in previous office action required election of one of the following groups:

I. Claims 1, 3-4, 8-9, 11-13, drawn to a bioactive MF3 polypeptide or a functional derivative thereof, a method of using said polypeptide, and a composition comprising said polypeptide.

II. Claims 2,5-7, and 14-15, drawn to an isolated DNA, a vector and cell/plant comprising said DNA

III. Group III, claim 10, drawn to a method of isolating and purifying an MF3 polypeptide from bacterial cells.

Applicant has provisionally elected Group II, but maintains that Groups I-III relate to a single general invention concept. This becomes specifically clear in the light of the currently amended claims and the arguments below.

In previous office action Examiner stated that the inventions of Groups I-III lack the same or corresponding special technical features for the following reasons:

The bioactive polypeptide derivative or functional fragment of claim 1 and a method of using it to protect plants are taught in the prior art as evidenced by Dzhavakhia et al (US 6,528,480B1). Examiner stated that Dzhavakhia teaches an isolated polypeptide from

bacteria that protects plants from against pathogen infections, and said polypeptide is considered an active an functional fragment of Applicant's SEQ ID NO: 1. Examiner stated that there is no special technical feature that links the polypeptide of Group I to the DNA of group II or the method of isolating the polypeptide of Group III.

Applicant objected Examiner's statement for the following reasons:

1) The protein structure of MF2 disclosed by Dzhavakhia et al. in US 6,528,480B1 and MF3 disclosed here do not have any obvious sequence homologies. The only common feature is that they are both thermostable. (Page 4, line 25 of the specification).

2) The MF2 polypeptide has a molecule weight of 7,239 daltons, while the MF3 of the instant application has a molecule weight of 17,600 daltons (page 4, line 29 of the specification).

3) Dzhavakhia et al. US 6,528,480B1 disclose a protein called MF2 derived from *Bacillus thuringiensis*, while the current application discloses a protein called MF3 derived from *Pseudomonas fluorescence.* Thus the origin of the proteins is completely different.

4) MF3 polypetide disclosed in this application has a structure that resembles the enzyme peptidyl-prolyl *cis-trans* isomerase SlyD (page 5 line 3 of the specification) while MF2 disclosed in US 6,528,480B1 has a structure that resembles cold shock proteins (column II line 40).

Applicant maintains that there is no basis to allege that the MF2 polypeptide of Dzhavakhia et al in US 6,528,480B1 would be an active or functional fragment of currently disclosed SEQ ID NO: 1. There is no basis to allege any kind of functional similarity of the two proteins and there is no obvious sequence homology between the two polypeptides. A polypeptide cannot be an active or functional fragment of another polypeptide, if there is no homology between the polypeptides.

Moreover, applicant has amended claim 1 now so that it provides the sequences of the active fragments, i.e. SEQ ID NO: 3 and SEQ ID NO: 4. These sequences and their active nature are disclosed in the original application in Example 18.

In the previous restriction requirement, Examiner stated that the special technical features of Group I that are not recited in any of the other groups are considered to be a bioactive polypeptide and a method of using said polypeptide with carrier molecules. The special technical features of Group II were considered to be an isolated DNA, a vector and transgenic plant/cell. The special technical features of Group III were considered to be cultivating a microbial strain, fractioning and gel electrophoresis steps. In the reply to previous office action, applicant amended claims 2 and 10 so that bioactive polypeptide became technical feature of each claim group. Now applicant has amended claim 2 with the amino acid sequence of the bioactive polypeptide, whereby applicant believes Group I and Group II claims should be read as one group.

Based on this, the applicant respectfully petitions review of the restriction requirement and withdrawal of the previously issued requirement for restriction. Dzhavakhia et al in US 6,528,480 does not teach a polypeptide that could be an active or functional fragment of SEQ ID NO: 1 as claimed in claim 1, there is a special technical feature that links the polypeptide of Group I to the DNA of Group II or to the method of isolating a polypeptide of Group III.

Sequence Listing

Examiner states that the specification on page 33 (lines 1-2, 4-5) and 36 (lines 22-23), recites sequences with not sequence identifier. Applicant has amended the specification by identifying the sequences on pages 33 and 36. Sequences on page 33 were listed on the original sequence listing as SEQ ID NO: 3 and SEQ ID NO:4, but the sequence identificators were missing on page 33. The primer sequences as disclosed on page 36

have now been identified as SEQ ID NO: 5 and SEQ ID NO: 6. These primer sequences were listed on the original sequence listing.

Applicant has amended page 34 with sequence identifiers SEQ ID NO: 7 and SEQ ID NO: 8 after the primer sequences disclosed. These sequences have been amended also into the replacement Sequence Listing that is attached herein.

Applicant has also amended SEQ ID NO1 and SEQ ID NO: 2 identifiers on page 6 and page 34. These sequences were in the original sequence listing, but applicant felt the specification would be clearer if the identifiers are mentioned in appropriate places in the specification too.

Information Disclosure Statement

Applicant acknowledges that Examiner has only considered references cited on form PTO-892.

Claim objections

Claims 2, 5-7 and 14-15 are objected to for depending upon non-elected claim1. Applicant has amended claim 2 so as to stand alone. Claims 5-7 and 14-15 are dependent on ultimately on claim 2.

Claim rejection under 35 USC paragraph 112

Claims 2, 5-7 and 14-15 are rejected under 35 USC 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 2 is indefinite in the recitation of 'bioactive' polypeptide and 'functional derivative' which are not clearly defined in the specification. Examiner states that the

terms are open to individual interpretations. Dependent claims 5-7 and 14-15 are included in the rejection because they do not obviate the rejection.

The term 'bioactive' is a common term in the field of peptide research. The term means 'having a capacity to interact with a living tissue or system'. Applicant attaches here a printout of yourdictionary.com where the term has been defined. One skilled in the art would know the meaning of the term and therefore the term is not open to individual interpretations.

Examiner stated that Applicant has not provided guidance for how to identify or obtain all the DNA sequences encoding polypetides having both the structural and functional limitations as recited in the claims.

In Example 18 applicant has identified polypeptide fragments SEQ ID NO3 and SEQ ID NO: 4 as having similar protective properties as the full length polypeptide SEQ ID NO: 1. These fragments, as disclosed o page 32 line 30-35 consist of regions 29-85 and 105-149, respectively, of the full 161 amino acid long MF3 polypeptide. Applicant has amended claim 1, so that it limits the active fragments to these specific polypeptide sequences.

Applicant believes that the rejection under 112 second paragraph is no more relevant in light of the amended claims and the above arguments.

Claim Rejection under 35 USC 112

Claims 2, 5-7 and 14-15 are rejected under 35 USC 112, first paragraph, because the specification, while being enabling for an isolated DNA sequence encoding SEQ ID NO: 1, a vector comprising said DNA sequence, host/cell plant transformed with said vector, does not reasonably provide enablement for an isolated DNA sequence encoding a

bioactive fragment or functional derivative SEQ ID NO: 1 or a fragment of SEQ ID NO:2.

Applicant has amended claim 2, so as to limit it to SEQ ID NO: 2. Applicant has also amended a new claim 16, claiming a DNA sequence encoding active polypeptide fragments SEQ ID NO: 3, and SEQ ID NO: 4.

Applicant believes that the claims are now allowable and the rejection is moot.

Written Description

Claims 2, 5-7 and 14-15 are rejected under 35 USC 112, first paragraph, as failing to comply with the written description requirement. Examiner states that the claims are drawn to an isolated DNA sequence according to SEQ ID NO:2, or fragment thereof, encoding the polypeptide MF3 of SEQ ID NO:1 or its bioactive fragment or functional derivative thereof, wherein said DNA fragment may contain degenerate codons; a vector comprising the DNA; a transgenic plant or plant cell culture comprising the vector; a host cell stably transformed or trasfected with the vector; said transgenic plant or plant cell culture having resistance against diseases caused by specific pathogens. Examiner states that the specification in contrast describes an isolated DNA sequence encoding SEQ ID NO: 1, a vector comprising said DNA sequence, host cell/plant stably transformed with said vector.

Examiner states that the specification does not describe the composition and structure of an active fragment, a fragment of a functional derivative of SEQ ID NO: 1 or 2. Examiner further states that no description is provided for a polypeptide or DNA other than SEQ ID NO1 or 2.

Applicant points out that Example 18 discloses SEQ ID NO: 3 and SEQ ID NO: 4, which are fragments of the full length MF3 polypeptide. The example shows that these sequences possess similar functional characters as the full length sequence. Applicant

has amended claim 1, so as to include SEQ ID NO: 3 and 4. Applicant has also amended claim 2, so as to claim only SEQ ID NO: 1. Applicant has amended new claim 16 to claim the isolated DNA sequences encoding SEQ ID NO: 3 and SEQ ID NO: 4 polypeptides.

Applicant believes that the claims are now allowable and fully enabled by the description.

Claim rejection under 35 USC 102

Examiner rejects claims 2, 5-7 and 14-15 under 35 USC 102(b) as being anticipated by Dzhavakhia et al (WO97/05165). Examiner states the Dzhavakhia et al. teach an isolated DNA encoding a polypeptide having antifungal and antiviral activity; a vector comprising said DNA, plant cell and plants stably transformed with said vector, wherein the plants exhibit resistance to *Phytophtora infestans* and TMV and PVX viruses.

Examiner states that the polypeptide encoded by the prior DNA would be a bioactive fragment or functional derivative of Applicant's SEQ ID NO: 2. Applicant has pointed already above (see restriction requirement) that there is no homology between the polypeptide sequence of Dzhavakhia et al. and currently claimed SEQ ID NO: 2. It is difficult to imagine how a polypeptide could be a bioactive fragment or functional derivative of another polypeptide if the polypeptide sequences do not have any obvious homology. Applicant genuinely believes that this rejection is unreasonable.

Examiner states further, that the prior art DNA sequence also represents a fragment of SEQ ID NO: 2, since no specific definitions or other structural characteristics that would distinguish the claimed DNA/polypeptide from the prior art DNA/polypeptide is disclosed. Again applicant cannot understand the basis for this rejection. Dzavakhia discloses the amino acid sequence of the prior art polypeptide and the current application discloses the sequence of the MF3 polypeptide (SEQ ID NO: 2). Moreover, the current application and the amended claims disclose functional derivatives having SEQ ID NO: 3

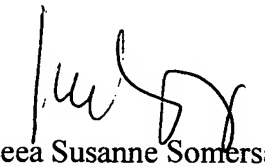
and SEQ ID NO:4. Therefore, specific definitions have been disclosed to distinguish the claimed DNA/polypeptide from the prior art DNA/polypeptide.

Applicant is of the opinion that the rejection does not have any basis. The DNA sequence and the polypeptide sequence disclosed in Dzhavakhia patent originates from *Bacillus thuringiensis,* while the current sequences are derived from *Pseudomonas fluorescence.* The polypeptide sequences do not have any obvious homologies, whereby one is not a fragment of the other. Moreover, MF3 polypetide disclosed in this application has a structure that resembles the enzyme peptidyl-prolyl *cis-trans* isomerase SlyD, while MF2 disclosed in US 6,528,480B1 has a structure that resembles cold shock proteins (column II line 40). Therefore, applicant is of the opinion that the rejection is moot.

CONCLUSION

Applicant respectfully request withdrawal of the restriction requirement and allowance of the claims as now amended. None of the amendments made here do add any new matter into the application.

DODDS AND ASSOCIATES

By: 
Leea Susanne Somersalo
Reg No. L0092

cc. file
Dr. Vitaly Dzavakhia
Dr. Timo Korpela

YourDictionary.com The last word in words

bioactive

Related Forms · Usage Examples

bioactive definition

bio·ac·tive (-ak'tiv)

adjective

having a capacity to interact with a living tissue or system

bioactive related forms

bio'·ac·tiv'·ity (-ak tiv'□ tē) *noun*

bioactive usage examples

modifies a noun

- peptide: The ultimate aim is the ability to develop enzymes, protein ligands and bioactive peptides to order.
- compound: The chapter ends with assessments of the evidence on a large number of bioactive compounds mostly found in plant foods.
- molecule: This will enable us to generate the complex molecular architecture of important bioactive molecules in a single step.
- substance: Experiments are performed under control conditions and in the presence of the desired bioactive substance in the same patch.
- glass: Bioactive glasses and machinable glass-ceramics are available under a number of trade names.
- component: Certain bioactive components in whey protein may be responsible for the cholesterol reduction however additional research is needed in this area.

modifying another word

- potentially: We are developing a new method of screening potentially bioactive molecules which uses a combination of enzymes to select active structures.

Browse dictionary entries near *bioactive*

‹ bioacoustics
‹ bioaccumulation
‹ bio-
‹ bio
‹ binucleate
‹ binturong
‹ bint
‹ binomial theorem
‹ binomial distribution

bioassay ›
bioastronautics ›
bioavailability ›
biocatalyst ›
biocenosis ›
biochemical oxygen demand ›
biochemistry ›
biocidal ›
biocide ›

‹ binomial coefficient bioclean ›